SEQUENCE LISTING

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OKI, HIROYUKI
YAMAGUCHI, HIROTAKA

<120> METHOD FOR TRANSFORMING PLANT, THE RESULTANT PLANT AND GENE THEREOF

<130> 55022-DIV (71526)

<140> 10/625,821
<141> 2003-07-22

<150> 09/646,825
<151> 2000-09-22

<150> JP/10-96637
<151> 1998-03-24

<160> 38

<170> PatentIn Ver. 2.1

<210> 1
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<222> (20)..(2077)

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                    Met Val Arg Thr Arg Val Leu Phe Cys Leu Phe
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atc tct ttc ttc gct aca gtc caa tcg agc gct aca ctc atc tcc act   100
Ile Ser Phe Phe Ala Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr
             15                  20                  25

tca tgc att tct cag gct gca ctg tac cag ttc gga tgc tca agc aag   148
Ser Cys Ile Ser Gln Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys
         30                  35                  40

tca aag tct tgc tac tgc aag aac atc aat tgg ctc gga agc gtc act   196
Ser Lys Ser Cys Tyr Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr
     45                  50                  55

gca tgc gct tat gag aac tcc aaa tct aac aag act ctg gac tcc gct   244
Ala Cys Ala Tyr Glu Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala
 60                  65                  70                  75
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ttg atg aaa ctt gcc agc caa tgc tca agt atc aag gtt tac aca ctg   292
Leu Met Lys Leu Ala Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu
                 80                  85                  90

gag gac atg aag aac atc tac ctt aat gca agt aac tac ctt cgc gct   340
Glu Asp Met Lys Asn Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala
             95                 100                 105

cct gag aaa tcc gat aag aag aca gtt gtt tca caa ccg ttg atg gca   388
Pro Glu Lys Ser Asp Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala
        110                 115                 120

aat gag acg gcc tat cac tac tac tat gag gaa aac tat ggg atc cac   436
Asn Glu Thr Ala Tyr His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His
    125                 130                 135

ttg aat ttg atg cga tct caa tgg tgc gca tgg ggc ctc gtc ttc ttc   484
Leu Asn Leu Met Arg Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe
140                 145                 150                 155

tgg gtc gca gtc ctt acc gcc gca act atc ttg aac att ctc aaa cgc   532
Trp Val Ala Val Leu Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg
                160                 165                 170

gta ttc ggc aag aac att atg gca aat tct gtt aag aag tct ctt atc   580
Val Phe Gly Lys Asn Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile
            175                 180                 185

tac cca agc gtt tac aaa gac tac aac gag aga act ttc tat ctt tgg   628
Tyr Pro Ser Val Tyr Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp
        190                 195                 200

aaa cgt ttg cca ttc aac ttt aca act cga ggc aaa gga ctc gta gtt   676
Lys Arg Leu Pro Phe Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val
    205                 210                 215

ctt atc ttt gtc att ctg act att ctc tca ctc tct ttc gga cat aac   724
Leu Ile Phe Val Ile Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn
220                 225                 230                 235

atc aag ttg cca cat cct tac gat aga cct aga tgg aga aga tca atg   772
Ile Lys Leu Pro His Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met
                240                 245                 250

gca ttc gtc tca cgc cgt gct gac ttg atg gca atc gct ctt ttc ccc   820
Ala Phe Val Ser Arg Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro
            255                 260                 265

gtg gtg tac ctt ttc ggt atc cgg aac aac ccc ttc atc cca atc acc   868
Val Val Tyr Leu Phe Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr
        270                 275                 280

gga ttg agc ttt agt act ttc aac ttt tac cac aaa tgg tca gca tac   916
Gly Leu Ser Phe Ser Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr
    285                 290                 295
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gtc tgc ttc atg tta gcc gtc gtc cat tca atc gtt atg acc gct tca   964
Val Cys Phe Met Leu Ala Val Val His Ser Ile Val Met Thr Ala Ser
300                 305                 310                 315

gga gtt aaa cga gga gta ttc cag tct ctt gta agg aaa ttc tac ttc   1012
Gly Val Lys Arg Gly Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe
                320                 325                 330

aga tgg gga ata gta gcc aca att ctt atg tcc atc atc att ttc cag   1060
Arg Trp Gly Ile Val Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln
            335                 340                 345

tcc gag aag gtc ttc agg aac cga ggt tat gaa atc ttc tta ctt att   1108
Ser Glu Lys Val Phe Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile
        350                 355                 360

cac aaa gcc atg aac atc atg ttt atc ata gct atg tat tac cat tgc   1156
His Lys Ala Met Asn Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys
    365                 370                 375

cac aca cta gga tgg atg ggc tgg atc tgg tcc atg gct ggc atc ctc   1204
His Thr Leu Gly Trp Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu
380                 385                 390                 395

tgc ttc gac agg ttc tgc cga att gta cgt atc atc atg aac gga ggt   1252
Cys Phe Asp Arg Phe Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly
                400                 405                 410

ctt aag acc gcc act ttg tcg acc aca gat gat tct aac gtt atc aag   1300
Leu Lys Thr Ala Thr Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys
            415                 420                 425

atc tct gtc aag aag cct aag ttc ttc aag tat caa gtg gga gca ttt   1348
Ile Ser Val Lys Lys Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe
        430                 435                 440

gcc tat atg tac ttt ctt tca cca aaa tca gcc tgg ttc tac agt ttt   1396
Ala Tyr Met Tyr Phe Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe
    445                 450                 455

caa tct cat ccc ttc aca gtc cta tca gaa agg cac aga gat cct aac   1444
Gln Ser His Pro Phe Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn
460                 465                 470                 475

aac cca gat caa cta act atg tac gtc aaa gct aac aag ggc att acg   1492
Asn Pro Asp Gln Leu Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr
                480                 485                 490

aga gta ctt ctt agc aaa gtt cta agc gct cca aac cat acc gtt gat   1540
Arg Val Leu Leu Ser Lys Val Leu Ser Ala Pro Asn His Thr Val Asp
            495                 500                 505

tgc aag att ttc tta gag gga cca tat ggc gta act gtc cct cac att   1588
Cys Lys Ile Phe Leu Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile
        510                 515                 520
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gcc aaa ctt aag aga aat cta gta gga gta gct gcg ggc ctc ggc gtg   1636
Ala Lys Leu Lys Arg Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val
    525                 530                 535

gca gcc atc tac ccc cat ttc gta gaa tgc ctt aga ttg cct agc act   1684
Ala Ala Ile Tyr Pro His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr
540                 545                 550                 555

gat caa ctg cag cac aag ttc tac tgg atc gtc aac gac ctt agt cac   1732
Asp Gln Leu Gln His Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His
                560                 565                 570

ctt aag tgg ttc gaa aac gag cta caa tgg ctt aag gag aaa tct tgt   1780
Leu Lys Trp Phe Glu Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys
            575                 580                 585

gaa gtc tct gtc atc tac act ggg tca tca gtg gag gat aca aac tca   1828
Glu Val Ser Val Ile Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser
        590                 595                 600

gat gag tcc act aag ggt ttc gat gac aag gaa gaa tct gaa atc acc   1876
Asp Glu Ser Thr Lys Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr
    605                 610                 615

gta gaa tgc ctt aac aag agg cca gac ctc aaa gag cta gtg aga tca   1924
Val Glu Cys Leu Asn Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser
620                 625                 630                 \ 635

gag atc aaa ttg tca gaa ctc gag aac aac aac atc act ttc tac tca   1972
Glu Ile Lys Leu Ser Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser
                640                 645                 650

tgc gga cca gcg act ttc aat gac gac ttt agg aat gca gtt gta caa   2020
Cys Gly Pro Ala Thr Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln
            655                 660                 665

ggt atc gat tct agt ctg aag ata gat gtc gaa cta gag gag gag agt   2068
Gly Ile Asp Ser Ser Leu Lys Ile Asp Val Glu Leu Glu Glu Glu Ser
        670                 675                 680

ttt act tgg taagagctca agctt                                     2092
Phe Thr Trp
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<210> 2
<211> 686
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<220>
<223> Description of Artificial Sequence: Synthetic saccharomyces cerevisiae

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              20                  25                  30

Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys Ser Lys Ser Cys Tyr
          35                  40                  45

Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr Ala Cys Ala Tyr Glu
      50                  55                  60

Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala Leu Met Lys Leu Ala
 65                  70                  75                  80

Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu Glu Asp Met Lys Asn
                 85                  90                  95

Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala Pro Glu Lys Ser Asp
            100                 105                 110

Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala Asn Glu Thr Ala Tyr
        115                 120                 125

His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His Leu Asn Leu Met Arg
    130                 135                 140

Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe Trp Val Ala Val Leu
145                 150                 155                 160

Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg Val Phe Gly Lys Asn
                165                 170                 175

Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr
            180                 185                 190

Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe
        195                 200                 205

Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile
    210                 215                 220

Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
225                 230                 235                 240

Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met Ala Phe Val Ser Arg
                245                 250                 255

Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro Val Val Tyr Leu Phe
            260                 265                 270

Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr Gly Leu Ser Phe Ser
        275                 280                 285

Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr Val Cys Phe Met Leu
    290                 295                 300

Ala Val Val His Ser Ile Val Met Thr Ala Ser Gly Val Lys Arg Gly
305                 310                 315                 320
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Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe Arg Trp Gly Ile Val
                325                 330                 335

Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln Ser Glu Lys Val Phe
            340                 345                 350

Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile His Lys Ala Met Asn
        355                 360                 365

Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys His Thr Leu Gly Trp
    370                 375                 380

Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu Cys Phe Asp Arg Phe
385                 390                 395                 400

Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly Leu Lys Thr Ala Thr
                405                 410                 415

Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys Ile Ser Val Lys Lys
            420                 425                 430

Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe Ala Tyr Met Tyr Phe
        435                 440                 445

Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe Gln Ser His Pro Phe
    450                 455                 460

Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn Asn Pro Asp Gln Leu
465                 470                 475                 480

Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr Arg Val Leu Leu Ser
                485                 490                 495

Lys Val Leu Ser Ala Pro Asn His Thr Val Asp Cys Lys Ile Phe Leu
            500                 505                 510

Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile Ala Lys Leu Lys Arg
        515                 520                 525

Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val Ala Ala Ile Tyr Pro
    530                 535                 540

His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr Asp Gln Leu Gln His
545                 550                 555                 560

Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His Leu Lys Trp Phe Glu
                565                 570                 575

Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys Glu Val Ser Val Ile
            580                 585                 590

Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser Asp Glu Ser Thr Lys
        595                 600                 605

Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr Val Glu Cys Leu Asn
    610                 615                 620
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Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser Glu Ile Lys Leu Ser
625 630 635 640

Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser Cys Gly Pro Ala Thr
645 650 655

Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln Gly Ile Asp Ser Ser
660 665 670

Leu Lys Ile Asp Val Glu Leu Glu Glu Ser Phe Thr Trp
675 680 685

<210> 3
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 3
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<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 4
acacttatta gcacttcatg tatt 24

<210> 5
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
gaattctcta gactccacca tggttagaac cagagtcctt ttctgcctct tcatctcttt 60
cttcgctaca gtccaatcga gcg 83

<210> 6
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
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ttcggatgct caagcaagtc aaa 83

<210> 7
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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caagcaagtc aaagtcttgc tactgcaaga acatcaattg gctcggaagc gtcactgcat 60
gcgcttatga gaactccaaa tct 83

<210> 8
<211> 83
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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tccagtgtgt aaaccttgat acttgagcat tggctggcaa gtttcatcaa agcggagtcc 60
agagtcttgt tagatttgga gtt 83

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
tgtcttctta tcggatttct caggagcgcg aaggtagtta cttgcattaa ggtagatgtt 60
cttcatgtcc tccagtgtgt aaa 83

<210> 10
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
ggatcccata gttttcctca tagtagtagt gataggccgt ctcatttgcc atcaacggtt 60
gtgaaacaac tgtcttctta tcg 83

<210> 11

<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
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tcgcagtcct taccgccgca 80

<210> 12
<211> 80
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 12
ccttaccgcc gcaactatct tgaacattct caaacgcgta ttcggcaaga acattatggc 60
aaattctgtt aagaagtctc 80

<210> 13
<211> 80
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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ctttggaaac gtttgccatt 80

<210> 14
<211> 80
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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taaagttgaa tggcaaacgt 80

<210> 15
<211> 80
<212> DNA
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<223> Description of Artificial Sequence: Primer

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ccgaaagaga gtgagagaat 80

<210> 16
<211> 80
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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gtgagacgaa tgccattgat 80

<210> 17
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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acaaatggtc agcatacgtc tgc 83

<210> 18
<211> 83
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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aaacgaggag tattccagtc tct 83

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<211> 83
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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tgtccatcat cattttccag tcc 83

<210> 20
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
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aagaccttct cggactggaa aat 83

<210> 21
<211> 83
<212> DNA
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<223> Description of Artificial Sequence: Primer

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<210> 22
<211> 83
<212> DNA
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<223> Description of Artificial Sequence: Primer

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<210> 23
<211> 82
<212> DNA
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<223> Description of Artificial Sequence: Primer

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gtatcaagtg ggagcatttg cc 82

<210> 24
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 25
<211> 82
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<220>
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gtcaaagcta acaagggcat ta 82

<210> 26
<211> 82
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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gtactctcgt aatgcccttg tt 82

<210> 27
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
ggcccgcagc tactcctact agatttctct taagtttggc aatgtgaggg acagttacgc 60
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<210> 28
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
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<210> 29
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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gagctacaat ggcttaa 77

<210> 30
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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ggatacaaac tcagatg 77

<210> 31
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
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aatgccttaa caagagg 77

<210> 32
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
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tctggcctct tgttaag 77

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<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
cgataccttg tacaactgca ttcctaaagt cgtcattgaa agtcgctggt ccgcatgagt 60
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<210> 34
<211> 77
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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agaatcgata ccttgta 77

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<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
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<210> 36
<211> 2059
<212> DNA
<213> Saccharomyces cerevisiae

<400> 36
atggttagaa cccgtgtatt attctgctta tttatatctt tttttgctac ggttcaatcg 60
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tctagtaaat ctaaaagttg ctactgtaaa aacatcaatt ggctgggttc agtgacagca 180
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actgcagcca ctatcttgaa cattctgaaa agggtgtttg gtaagaacat catggcaaac 540
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tatttatgga agcgtctacc atttaatttt acaactcgag gcaagggtct cgtcgtatta 660
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gaa cga act ttt tat tta tgg aag cgt cta cca ttt aat ttt aca act   96
Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe Asn Phe Thr Thr
             20                  25                  30

cga ggc aag ggt ctc gtc gta tta att ttt gtt att ttg act ata tta   144
Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile Leu Thr Ile Leu
         35                  40                  45

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Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe Asn Phe Thr Thr
             20                  25                  30
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Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile Leu Thr Ile Leu
          35                  40                  45

Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
     50                  55                  60
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